NM 5/10/02

➢ Please replace the paragraph on page 11, lines 14-24 ~~with the following paragraph:~~

IDC-A1,AMD,M

FIGS. 3A-3Z2 are a table of marker genes for central nervous system (CNS) tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (CNS) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 11, line 25 ~~through page 12, line 6 with the following paragraph:~~

FIGS. 4A-4S2 are a table of marker genes for colorectal tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (colorectal) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

IDC-A2,AMD,M

measure the amount of hybridization at each position on the microarray with an ~~Affymetrix~~ AFFYMETRIX® scanner (Affymetrix Inc., Santa Clara, Calif.). For each stimulus a time series of nucleic acid levels (C={C1,C2,C3, . . . Cn}) and a corresponding time series of nucleic acid levels (M={M1,M2,M3, . . . Mn}) in control medium in the same experiment as the stimulus is obtained. Quantitative data is then analyzed. Hybridization analysis using microarray is only one method for obtaining gene expression values. Other methods for obtaining gene expression values known in the art or developed in the future can be used with the present invention. Once the gene expression values are determined, the sample can be classified.

➢ Please replace the paragraph on page 27, lines 11-20 ~~with the following~~ paragraph:

IDC-A3,AMD

The present invention also features arrays, for example, microarrays that have a plurality of oligonucleotide probes involved in tumor development immobilized thereon. The oligonucleotide probe may be specific for one or more genes specific for a particular tumor or tumor class, selected from those genes described herein. Such genes can be obtained using their ~~GenBank~~ GENBANK® Accession Numbers identified in FIGS. 1A-1R2, FIGS. 2A-2T2, FIGS. 3A-3Z2, FIGS. 4A-4S2, FIGS. 5A-5M2, FIGS. 6A-6W2, FIGS. 7A-7D3, FIGS. 8A-8X2, FIGS. 9A-9C3, FIGS. 10A-10P2, FIGS. 11A-11O2, FIGS. 12A-12V2, FIGS. 13A-13N2, and FIGS. 14A-14A3. Methods for making oligonucleotide microarrays are well known in the art, and are described, for example, in WO 95/11995, the entire teachings of which are hereby incorporated by reference.

➢ Please replace the paragraph on page 28, lines 3-~~27~~ 12 ~~with the following~~ paragraph: NM 5/10/06

IDC-A4,AMD,M

Approximately 300 human tumor and normal tissue specimens were identified and obtained or purchased from a variety of academic or commercial sources. These specimens represented 30 individual classes of tumor or normal tissue with each class containing between 5 and 20 samples. Total RNA was